Microbiol Resour Announc. 2020 Jul 30;9(31):e00570-20. doi: 10.1128/MRA.00570-20

Draft Genome Sequences of *Rhodotorula mucilaginosa* Strains Isolated from the International Space Station

Robert Daudu [a], Ceth W Parker [a], Nitin K Singh [a], Jason M Wood [a], Marilyne Debieu [b], Niamh B O'Hara [b,c], Christopher E Mason [d,e], Kasthuri Venkateswaran [a,✉]

Editor: Jason E Stajich[f]

Author information Article notes Copyright and License information

PMCID: PMC7393961 PMID: 32732232

The whole-genome sequences (WGS) of 28 isolates from the International Space Station were generated and identified as *Rhodotorula mucilaginosa*, a pigmented yeast that has been classified as an emerging human pathogen in recent times. These WGS enable the identification of genes responsible for synthesizing compounds with biological implications.

ABSTRACT

The whole-genome sequences (WGS) of 28 isolates from the International Space Station were generated and identified as *Rhodotorula mucilaginosa*, a pigmented yeast that has been classified as an emerging human pathogen in recent times. These WGS enable the identification of genes responsible for synthesizing compounds with biological implications.

ANNOUNCEMENT

Rhodotorula mucilaginosa of phylum *Basidiomycota* is found in soil, air, food, stool, and other environments (1) and produces carotenoids, making it easily identifiable by its distinctive pink, yellow, orange, or red colonies (2). Carotenoids are important for various biological activities, including vitamin A biosynthesis, enhancement of the immune system, reduction of the risk of various diseases (3), and protection from radiation (4). For these reasons, *R. mucilaginosa* carotenoids are used as food additives and hold pharmaceutical potential (5). *R. mucilaginosa,* which was previously considered to be nonpathogenic, has now been classified as an emerging pathogen (6, 7) and has been shown to colonize central venous catheters, causing fungemia due to biofilm formation (8).

Among the 28 recognized members of the genus *Rhodotorula* (9), *R. mucilaginosa* is the most common species isolated from the environment (7) and the most abundant yeast isolated from surfaces of the International Space Station (ISS) (10). The ability of this yeast to produce biofilms makes it very important to study ISS strains since the harsh conditions of the ISS (microgravity and radiation) were shown to enhance antimicrobial resistance and biofilm formation (11, 12). Due to their ability to form biofilms and colonize life support systems, such as water tanks and pipes containing clean water, characterization of whole-genome sequences (WGS) of *R. mucilaginosa* would allow for the development of countermeasures to eradicate this potential threat.

Samples were collected from ISS surfaces using premoistened polyester wipes (10). Each sample was aseptically transferred into 200 ml of phosphate-buffered saline, vigorously shaken, and concentrated using an InnovaPrep (Drexel, MO) CP-150 concentrated pipette. A 100-µl aliquot from each sample was plated onto potato dextrose agar (PDA) with 100 µg/ml chloramphenicol (25°C; 7 days). A single colony was obtained and restreaked onto PDA plates (25°C; 7 days), and a single colony was collected for DNA extraction. Genomic DNA was extracted by using a ZymoBIOMICS DNA MagBead kit (Zymo, Irvine, CA).

To acquire the WGS of these 28 fungal strains, shotgun libraries were prepared using the Illumina Nextera Flex protocol (13). Paired-end sequencing was performed on a NovaSeq 6000 S4 flowcell paired-end (PE) 2 × 150-bp platform. Quality analysis was performed with FastQC (v0.11.7) (14) to validate the quality of the raw sequencing data. For quality control, adapter trimming and quality filtering were performed using the software fastp (v0.20.0) (15), and then the cleaned sequences were assembled using SPAdes (v3.11.1) (16). Three functions of fastp were used, namely, correction of mismatches in overlapped regions of paired-end reads, trimming of autodetected adapter sequences, and quality trimming at the 5′ and 3′ ends. SPAdes ran using an option to reduce the number of mismatches and short indels in the final contigs, the automatic read coverage cutoff value, and the default values of k-mer sizes. To assess the assembly quality, the number of contigs, N_{50} values, median coverage, and the genome size were calculated using QUAST (v5.0.2) (17) (Table 1). The G+C content ranged between 60.53% and 60.55%. All other statistics are given in Table 1.

TABLE 1.

Genome statistics of *Rhodotorula mucilaginosa* isolated from various ISS environments during microbial tracking[a]

Sample name	GenBank accession no.	Raw sequence accession no.	Flight/ location	Location description	No. of contigs	Genome size (bp)	N_{50} (bp)	c
IF1SW-B1	JABBIR000000000	SRR11774209	F1-1	Cupola (node 3)	177	20,046,905	330,870	1
IF1SW-F2	JABBIH000000000	SRR11774205	F1-1	Cupola (node 3)	198	20,124,384	333,776	8
IF3SW-F2	JABBIG000000000	SRR11774204	F1-3	ARED (node 3)	201	20,117,457	333,691	9
IF4SW-B1	JABBIQ000000000	SRR11774208	F1-4	Dining table (node 1)	187	20,115,049	329,462	1
IF4SW-B2	JABBIP000000000	SRR11774197	F1-4	Dining table (node 1)	170	20,047,348	332,671	1
IF4SW-F2	JABBIF000000000	SRR11774203	F1-4	Dining table (node 1)	185	20,043,495	330,890	8
IF5SW-F1	JABBIE000000000	SRR11774202	F1-5	Zero G stowage rack	192	20,113,158	332,417	1
IF6SW-B2	JABBYN000000000	SRR11774188	F1-6	PMM port 1	179	20,045,004	359,523	1
IF6SW-F1	JABBID000000000	SRR11774201	F1-6	PMM port 1	180	20,050,344	331,252	1
IF7SW-B3	JABBIO000000000	SRR11774187	F1-7	Lab 3 overhead	192	20,045,846	339,159	1

Sample name	GenBank accession no.	Raw sequence accession no.	Flight/ location	Location description	No. of contigs	Genome size (bp)	N_{50} (bp)	c
IF8SW-B2	JABBIN000000000	SRR11774186	F1-8	Port crew quarters (node 2)	188	20,043,142	352,443	1
IF8SW-P2	JABBIM000000000	SRR11774185	F1-8	Port crew quarters (node 2)	192	20,113,185	319,608	1
IIF1SW-F1	JABBIC000000000	SRR11774200	F2-1	Cupola (node 3)	203	20,113,961	335,522	9
IIF2*SW-B1	JABBII000000000	SRR11774206	F2-2	WHC	184	20,052,772	275,091	1
IIF2SW-F1	JABBMW000000000	SRR11774199	F2-2	WHC	180	20,050,420	343,644	1
IIF2*SW-F1	JABBIA000000000	SRR11774194	F2-2	WHC	199	20,045,739	311,341	9
IIF4SW-F1	JABBMV000000000	SRR11774198	F2-4	Dining table (node 1)	178	19,988,416	334,586	6
IIF5SW-F2	JABBMU000000000	SRR11774196	F2-5	Zero G stowage rack	173	19,996,184	340,304	1
IIF6SW-B1	JABBMX000000000	SRR11774184	F2-6	PMM port 1	201	20,114,311	317,098	1
IIF6SW-B2	JABBIL000000000	SRR11774183	F2-6	PMM port 1	193	20,045,085	311,342	1
IIF6SW-F1	JABBYM000000000	SRR11774193	F2-6	PMM port 1	188	20,045,112	294,049	9
IIF8SW-B2	JABBIK000000000	SRR11774182	F2-8	Port crew quarters (node 2)	172	20,044,451	330,156	9

Sample name	GenBank accession no.	Raw sequence accession no.	Flight/ location	Location description	No. of contigs	Genome size (bp)	N_{50} (bp)	c
IIF8SW-B3	JABBIJ000000000	SRR11774207	F2-8	Port crew quarters (node 2)	175	20,050,813	328,275	1
IIF8SW-F1	JABBIB000000000	SRR11774195	F2-8	Port crew quarters (node 2)	173	20,047,674	343,393	1
IIFCSW-F1	JABBHZ000000000	SRR11774192	F2-FC	Field control wipe	188	20,117,057	331,823	1
IFCSG-B1	JABBHY000000000	SRR11774191	Ground CRV-5	Inside capsule CRV5 (FC)	177	20,050,250	321,788	1
IF1SG-B1	JABBHX000000000	SRR11774190	Ground CRV-5	Outside capsule CRV5 (L1)	176	20,053,156	335,912	1
IF3SG-B1	JABBHW000000000	SRR11774189	Ground CRV-5	Inside capsule CRV5 (L3)	185	20,046,360	317,139	1

Open in a new tab

[a]Abbreviations: F1 and F2, flight 1 and 2, respectively; ARED, advanced resistive exercise device; WHC, waste and hygiene compartment; PMM, permanent multipurpose module; CRV, crew resupply vehicle; FC, field control.

Data availability.

This whole-genome shotgun project has been deposited at DDBJ/ENA/GenBank under the accession numbers given in Table 1 (BioProject no. PRJNA625575). The version described in this paper is the first version.

ACKNOWLEDGMENTS

Part of the research described in this publication was carried out at the Jet Propulsion Laboratory, California Institute of Technology, under a contract with NASA.

We thank astronauts Captain Terry Virts and Commander Jeffrey Williams for collecting samples aboard the ISS and the Implementation Team at NASA Ames Research Center for coordinating this effort. We also thank Ryan Kemp of Zymo Corporation for extracting DNA and Dan Butler of Cornell Medicine for generating shotgun sequencing using NovaSeq. R.D. thanks Wei-Jen Lin for providing guidance and directing R.D. to undertake research at JPL.

Government sponsorship is acknowledged. This research was funded by 2012 Space Biology NNH12ZTT001N grant no. 19-12829-26 under Task Order NNN13D111T award to K.V., which also funded a postdoctoral fellowship for C.W.P., a JPL graduate fellowship to R.D., and a subcontract to Biotia, Inc.

REFERENCES

1. Hazen KC. 1995. New and emerging yeast pathogens. Clin Microbiol Rev 8:462–478. doi: 10.1128/CMR.8.4.462. [DOI] [PMC free article] [PubMed] [Google Scholar]

2. Gan HM, Thomas BN, Cavanaugh NT, Morales GH, Mayers AN, Savka MA, Hudson AO. 2017. Whole genome sequencing of *Rhodotorula mucilaginosa* isolated from the chewing stick (*Distemonanthus benthamianus*): insights into *Rhodotorula* phylogeny, mitogenome dynamics and carotenoid biosynthesis. PeerJ 5:e4030. doi: 10.7717/peerj.4030. [DOI] [PMC free article] [PubMed] [Google Scholar]

3. Mata-Gómez LC, Montañez JC, Méndez-Zavala A, Aguilar CN. 2014. Biotechnological production of carotenoids by yeasts: an overview. Microb Cell Fact 13:12. doi: 10.1186/1475-2859-13-12. [DOI] [PMC free article] [PubMed] [Google Scholar]

4. Cortes AG, Vásquez JAG, Díaz YCA, Castrillón MR. 2020. Effects of cellular stress on pigment production in *Rhodotorula mucilaginosa*/*alborubescens* AJB01 strain from the Caribbean region of Colombia. bioRxiv doi: 10.1101/2020.05.20.107201. [DOI]

5. Kaur B, Chakraborty D, Kaur H. 2019. Production and stability analysis of yellowish pink pigments from *Rhodotorula rubra* MTCC 1446. Internet J Micobiol 7:1. [Google Scholar]

6. Miceli MH, Díaz JA, Lee SA. 2011. Emerging opportunistic yeast infections. Lancet Infect Dis 11:142–151. doi: 10.1016/S1473-3099(10)70218-8. [DOI] [PubMed] [Google Scholar]

7. Wirth F, Goldani LZ. 2012. Epidemiology of *Rhodotorula*: an emerging pathogen. Interdiscip Perspect

Infect Dis 2012:465717. doi: 10.1155/2012/465717. [DOI] [PMC free article] [PubMed] [Google Scholar]

8. Braun DK, Kauffman CA. 1992. *Rhodotorula* fungaemia: a life-threatening complication of indwelling central venous catheters. Mycoses 35:305–308. doi: 10.1111/j.1439-0507.1992.tb00882.x. [DOI] [PubMed] [Google Scholar]

9. Kurtzman C, Fell JW. 1998. The yeasts—a taxonomic study. Elsevier, Amsterdam, The Netherlands. [Google Scholar]

10. Checinska Sielaff A, Urbaniak C, Mohan GBM, Stepanov VG, Tran Q, Wood JM, Minich J, McDonald D, Mayer T, Knight R, Karouia F, Fox GE, Venkateswaran K. 2019. Characterization of the total and viable bacterial and fungal communities associated with the International Space Station surfaces. Microbiome 7:50. doi: 10.1186/s40168-019-0666-x. [DOI] [PMC free article] [PubMed] [Google Scholar]

11. Ichijo T, Yamaguchi N, Tanigaki F, Shirakawa M, Nasu M. 2016. Four-year bacterial monitoring in the International Space Station—Japanese Experiment Module “Kibo” with culture-independent approach. NPJ Microgravity 2:16007. doi: 10.1038/npjmgrav.2016.7. [DOI] [PMC free article] [PubMed] [Google Scholar]

12. Vaishampayan A, Grohmann E. 2019. Multi-resistant biofilm-forming pathogens on the International Space Station. J Biosci 44:125. doi: 10.1007/s12038-019-9929-8. [DOI] [PubMed] [Google Scholar]

13. Singh NK, Bezdan D, Checinska Sielaff A, Wheeler K, Mason CE, Venkateswaran K. 2018. Multi-drug resistant *Enterobacter bugandensis* species isolated from the International Space Station and comparative genomic analyses with human pathogenic strains. BMC Microbiol 18:175. doi: 10.1186/s12866-018-1325-2. [DOI] [PMC free article] [PubMed] [Google Scholar]

14. Andrews S. 2010. FastQC: a quality tool for high throughput sequence data. http://www.bioinformatics.babraham.ac.uk/projects/fastqc/ .

15. Chen S, Zhou Y, Chen Y, Gu J. 2018. fastp: an ultra-fast all-in-one FASTQ preprocessor. Bioinformatics 34:i884–i890. doi: 10.1093/bioinformatics/bty560. [DOI] [PMC free article] [PubMed] [Google Scholar]

16. Bankevich A, Nurk S, Antipov D, Gurevich AA, Dvorkin M, Kulikov AS, Lesin VM, Nikolenko SI, Pham S, Prjibelski AD, Pyshkin AV, Sirotkin AV, Vyahhi N, Tesler G, Alekseyev MA, Pevzner PA. 2012. SPAdes: a new genome assembly algorithm and its applications to single-cell sequencing. J Comput Biol 19:455–477. doi: 10.1089/cmb.2012.0021. [DOI] [PMC free article] [PubMed] [Google Scholar]

17. Gurevich A, Saveliev V, Vyahhi N, Tesler G. 2013. QUAST: quality assessment tool for genome assemblies. Bioinformatics 29:1072–1075. doi: 10.1093/bioinformatics/btt086. [DOI] [PMC free article]

Associated Data

This section collects any data citations, data availability statements, or supplementary materials included in this article.

Data Availability Statement

This whole-genome shotgun project has been deposited at DDBJ/ENA/GenBank under the accession numbers given in Table 1 (BioProject no. PRJNA625575). The version described in this paper is the first version.